PHDsec, PHDacc, PHDhtm, PHDtopology, PHDthreader and EvalSec. The transmembrane sequence regions were thus obtained.. A BLAST assisted template was then selected: Neuropeptide Y1 receptor (Homo sapiens). Trimethylamine was selected as the ligand. Using GRAMM, several possible binding domains were identified and corresponding polypeptides were generated. In Figure 5, (poly)peptide B1 SEQ. ID. No. 2 designed in accordance with the present invention illustrates better response for trimethylamine than another (poly)peptide Pb2 SEQ. ID. No. 3.

a3 Cont

REMARKS

Enclosed herewith is another paper copy of the sequence listing further to the request dated February 1, 2002. Also enclosed is another copy of the sequence listing in computer readable form. Both the content of the paper and the computer readable copy are the same and include no new matter.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "Version With Markings To Show Changes Made".

In the event that the present invention is not in a condition for allowance for any other reasons, the Examiner is respectfully invited to call the Applicant's representative at his Bloomfield Hills, Michigan office at (248) 540-4040 such that necessary action may be taken to place the application in a condition for allowance.

Respectfully submitted,

Tung & Associates

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Telephone: (248) 540-4040

RWT\kd
Enclosure: Computer readable disk

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In The Specification

Line 14 of page 3 has been amended as follows:

Figure 4 is an amino acid sequence for ORP P30955 SEQ. ID. NO. 1.

Line 16 of page 3 has been amended as follows:

Figure 5 is a table illustrating frequency changes resulting from attachment of ligands to a polypeptide SEQ. ID. No. 2 made in accordance with the present invention.

Lines 3, 10 and 11 of page 8 has been amended as follows:

A G-Protein Coupled Receptor database was accessed and the sequence of an ORP of known primary sequence, but unknown secondary and tertiary structures was retrieved (SWISS-PROT:P30955) as shown in Figure 4 SEQ. ID. No. 1. It consists of 330 amino acids and has a molecular weight of 35197 daltons. The

secondary structure was predicted and its accuracy verified through the use of MaxHom, PHDsec, PHDacc, PHDhtm, PHDtopology, PHDthreader and EvalSec. The transmembrane sequence regions were thus obtained.. A BLAST assisted template was then selected: Neuropeptide Y1 receptor (Homo sapiens). Trimethylamine was selected as the ligand. Using GRAMM, several possible binding domains were identified and corresponding polypeptides were generated. In Figure 5, (poly)peptide B1 SEQ. ID. No. 2 designed in accordance with the present invention illustrates better response for trimethylamine than another (poly)peptide Pb2 SEQ. ID. No. 3.